Full wwPDB X-ray Structure Validation Report ⓘ

Dec 4, 2023 – 07:53 am GMT

PDB ID	:	2W0K
Title	:	Crystal structure of the recombinant variable domain 6JAL2
Authors	:	Rudino-Pinera, E.; Gonzalezrubio-Garrido, P.; Horjales, E.
Deposited on	:	2008-08-19
Resolution	:	2.35 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

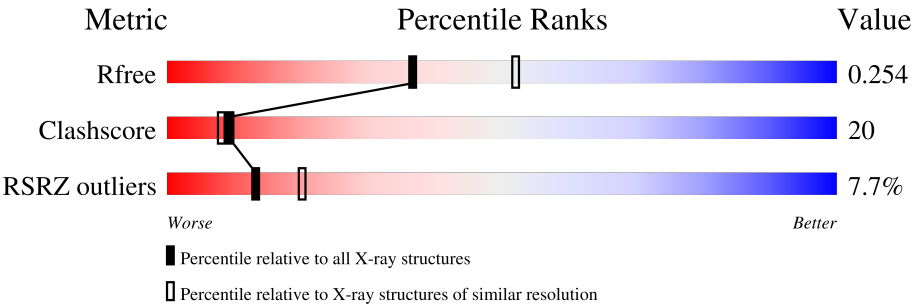
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1164 (2.36-2.36)
Clashscore	141614	1232 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	111	4% 68% 28%
1	B	111	12% 59% 34% 7%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1731 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called V1-22 PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	111	Total	C	N	O	S	0	0	0
			840	514	142	181	3			
1	B	111	Total	C	N	O	S	0	0	0
			840	514	142	181	3			

- Molecule 2 is water.

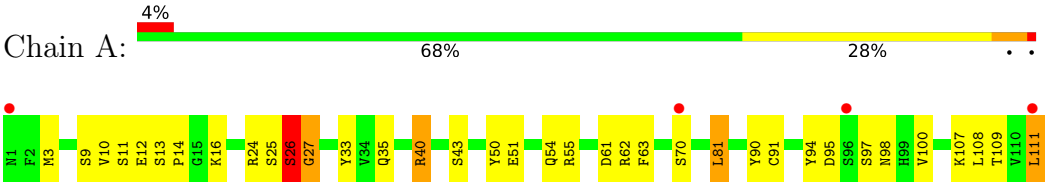
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	37	Total	O	0	0
			37	37		
2	B	14	Total	O	0	0
			14	14		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

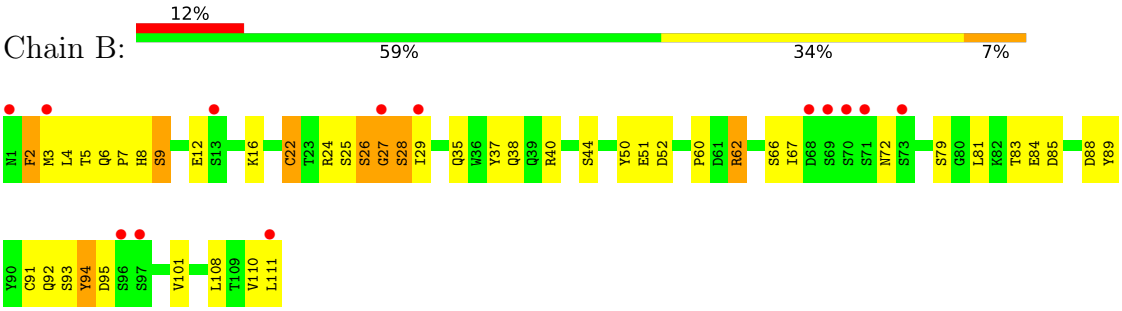
• Molecule 1: V1-22 PROTEIN

Chain A:



• Molecule 1: V1-22 PROTEIN

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 2 2	Depositor
Cell constants a, b, c, α, β, γ	71.27Å 71.27Å 95.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	22.63 – 2.35 22.52 – 2.35	Depositor EDS
% Data completeness (in resolution range)	86.0 (22.63-2.35) 86.1 (22.52-2.35)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.01 (at 2.36Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.209 , 0.242 0.209 , 0.254	Depositor DCC
R_{free} test set	441 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å^2)	45.1	Xtriage
Anisotropy	0.021	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 46.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	1731	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.74% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	1.54	6/857 (0.7%)	1.30	7/1163 (0.6%)
1	B	1.44	5/858 (0.6%)	1.25	6/1166 (0.5%)
All	All	1.49	11/1715 (0.6%)	1.27	13/2329 (0.6%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	2
1	B	0	4
All	All	1	6

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	94	TYR	CE1-CZ	9.42	1.50	1.38
1	A	91	CYS	CB-SG	-8.77	1.67	1.82
1	B	9	SER	C-N	8.14	1.52	1.34
1	A	26	SER	C-N	7.28	1.46	1.33
1	B	94	TYR	CE1-CZ	6.13	1.46	1.38
1	A	90	TYR	CZ-OH	5.96	1.48	1.37
1	A	43	SER	CB-OG	5.91	1.50	1.42
1	B	22	CYS	CB-SG	-5.50	1.72	1.81
1	B	9	SER	CB-OG	-5.30	1.35	1.42
1	B	37	TYR	CD1-CE1	5.16	1.47	1.39
1	A	111	LEU	C-OXT	-5.09	1.13	1.23

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	62	ARG	NE-CZ-NH1	-12.06	114.27	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	40	ARG	NE-CZ-NH1	-8.38	116.11	120.30
1	B	8	HIS	CB-CA-C	-7.85	94.70	110.40
1	A	62	ARG	NE-CZ-NH1	-7.03	116.79	120.30
1	A	40	ARG	NE-CZ-NH2	6.40	123.50	120.30
1	B	62	ARG	NE-CZ-NH2	6.24	123.42	120.30
1	A	61	ASP	CB-CG-OD1	5.84	123.56	118.30
1	B	2	PHE	N-CA-C	5.73	126.46	111.00
1	A	100	VAL	CG1-CB-CG2	5.66	119.96	110.90
1	A	81	LEU	CB-CG-CD1	-5.50	101.65	111.00
1	B	44	SER	N-CA-CB	-5.44	102.34	110.50
1	A	81	LEU	CA-CB-CG	5.40	127.72	115.30
1	B	88	ASP	CB-CG-OD1	5.32	123.09	118.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	26	SER	CA

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	26	SER	Mainchain
1	A	27	GLY	Mainchain
1	B	26	SER	Mainchain
1	B	27	GLY	Mainchain
1	B	28	SER	Mainchain
1	B	9	SER	Mainchain

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	840	0	786	31	0
1	B	840	0	787	35	0
2	A	37	0	0	1	0
2	B	14	0	0	1	0
All	All	1731	0	1573	64	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 20.

All (64) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:110:VAL:O	1:B:111:LEU:HB2	1.55	1.02
1:A:9:SER:C	1:A:10:VAL:N	2.29	0.86
1:A:14:PRO:HD3	1:A:111:LEU:OXT	1.85	0.77
1:B:12:GLU:HG3	1:B:16:LYS:HB3	1.67	0.76
1:A:9:SER:HA	1:A:10:VAL:N	2.00	0.76
1:B:40:ARG:NH2	1:B:84:GLU:O	2.18	0.75
1:A:9:SER:CA	1:A:10:VAL:N	2.49	0.75
1:B:12:GLU:O	1:B:111:LEU:N	2.17	0.72
1:B:2:PHE:HB3	1:B:26:SER:HB2	1.75	0.68
1:B:84:GLU:OE1	2:B:2014:HOH:O	2.12	0.66
1:B:26:SER:O	1:B:28:SER:N	2.29	0.66
1:A:9:SER:O	1:A:10:VAL:N	2.29	0.66
1:A:55:ARG:HD3	1:A:63:PHE:O	1.95	0.65
1:B:2:PHE:HE2	1:B:95:ASP:HA	1.63	0.64
1:A:40:ARG:HH11	1:A:40:ARG:HG3	1.62	0.64
1:A:26:SER:O	1:A:27:GLY:C	2.37	0.62
1:B:27:GLY:O	1:B:28:SER:HB3	2.02	0.59
1:A:81:LEU:HD21	1:A:108:LEU:HD21	1.84	0.58
1:B:110:VAL:O	1:B:111:LEU:CB	2.42	0.57
1:A:25:SER:O	1:A:26:SER:HB3	2.02	0.57
1:B:62:ARG:HG3	1:B:62:ARG:HH11	1.70	0.57
1:B:62:ARG:HG3	1:B:62:ARG:NH1	2.20	0.56
1:B:28:SER:HA	1:B:72:ASN:OD1	2.07	0.54
1:A:26:SER:HB3	1:B:60:PRO:HG3	1.91	0.53
1:A:12:GLU:HG3	1:A:16:LYS:HB2	1.91	0.52
1:B:51:GLU:O	1:B:52:ASP:HB2	2.11	0.51
1:B:4:LEU:HD13	1:B:91:CYS:SG	2.51	0.51
1:B:92:GLN:HA	1:B:101:VAL:O	2.10	0.51
1:A:70:SER:O	1:B:83:THR:OG1	2.28	0.51
1:B:83:THR:HA	1:B:110:VAL:HG11	1.93	0.51
1:B:2:PHE:CD1	1:B:24:ARG:HG3	2.47	0.50
1:B:12:GLU:CG	1:B:16:LYS:HB3	2.40	0.49
1:A:12:GLU:HG3	1:A:16:LYS:CB	2.43	0.49
1:A:95:ASP:OD2	1:A:95:ASP:C	2.51	0.48
1:A:107:LYS:HD3	1:A:107:LYS:C	2.34	0.48
1:B:93:SER:OG	1:B:94:TYR:N	2.46	0.48
1:B:62:ARG:NH1	1:B:85:ASP:OD2	2.47	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:ARG:HH11	1:A:40:ARG:CG	2.20	0.48
1:A:26:SER:O	1:A:27:GLY:O	2.32	0.47
1:B:66:SER:O	1:B:67:ILE:HD13	2.14	0.47
1:B:4:LEU:HD13	1:B:22:CYS:SG	2.56	0.45
1:B:35:GLN:HG3	1:B:50:TYR:HA	1.99	0.45
1:A:33:TYR:CD1	1:A:51:GLU:HA	2.53	0.44
1:B:111:LEU:HD12	1:B:111:LEU:HA	1.77	0.44
1:A:24:ARG:HG2	1:A:26:SER:O	2.18	0.43
1:A:13:SER:O	1:A:16:LYS:HB2	2.18	0.43
1:A:11:SER:HB3	1:A:109:THR:HB	1.99	0.43
1:A:97:SER:OG	2:A:2030:HOH:O	2.22	0.43
1:A:40:ARG:CG	1:A:40:ARG:NH1	2.80	0.43
1:B:6:GLN:HA	1:B:7:PRO:HD3	1.70	0.43
1:A:9:SER:O	1:A:10:VAL:CA	2.67	0.42
1:A:97:SER:O	1:A:98:ASN:HB2	2.19	0.42
1:A:3:MET:HB3	1:A:3:MET:HE2	0.87	0.42
1:A:11:SER:HA	1:A:109:THR:O	2.19	0.42
1:B:3:MET:HE3	1:B:25:SER:OG	2.19	0.42
1:B:29:ILE:O	1:B:29:ILE:HG13	2.20	0.42
1:B:38:GLN:HG3	1:B:89:TYR:CE2	2.55	0.41
1:B:81:LEU:HD21	1:B:108:LEU:HD21	2.02	0.41
1:A:35:GLN:HG3	1:A:50:TYR:HA	2.03	0.41
1:A:50:TYR:O	1:A:54:GLN:HB2	2.20	0.41
1:B:3:MET:O	1:B:24:ARG:HA	2.20	0.41
1:B:62:ARG:HB2	1:B:79:SER:O	2.21	0.41
1:B:5:THR:O	1:B:6:GLN:O	2.39	0.40
1:A:26:SER:HB2	1:A:27:GLY:H	1.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains (i)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	9:SER	C	10:VAL	N	2.29

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	111/111 (100%)	0.19	4 (3%) 42 55	38, 41, 44, 45	0
1	B	111/111 (100%)	0.57	13 (11%) 4 7	38, 41, 44, 45	0
All	All	222/222 (100%)	0.38	17 (7%) 13 20	38, 41, 44, 45	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	70	SER	6.7
1	B	1	ASN	4.9
1	A	111	LEU	4.3
1	B	96	SER	4.0
1	B	111	LEU	3.8
1	B	68	ASP	3.2
1	B	69	SER	3.2
1	B	97	SER	3.1
1	B	29	ILE	2.9
1	A	1	ASN	2.9
1	B	73	SER	2.8
1	A	96	SER	2.7
1	B	3	MET	2.6
1	A	70	SER	2.5
1	B	27	GLY	2.5
1	B	71	SER	2.2
1	B	13	SER	2.1

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.